

3406

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AAGCTTAAGGAGGTTAATCG ATG AAA AAA ACT GCT ATC GCT ATC GCT GTT

H A C met

i f RBS l

n l a

3 2 1

GCT CTG GCT GGT TTC GCT ACT GTT GCT CAG GCG GCG CCG AGA TCT

ala N

a r

l 2

AAA CAG GAA TTC GAG CTC GGT ACC CGG GGA TCC TCT AGA GTC GAC

E

C

O

I

S

a

C

I

K

p

h

I

X

m

a

I

B

a

m

I

X

b

a

I

S

a

l

I

CTG CAG GCA TGC

P S

s p

t h

1 1

3557

cI857

P<sub>R</sub>

RBS

7 NUCLEOTIDES

ClaI

NarI

MULTIPLE CLONING SEQUENCE

NarI-SphI

SphI

rno-INDEPENDENT  
TRANSCRIPTIONS  
TERMINATING  
SEQUENCES

pHD389

(4286 bp)

pUC19

ori

SIGNAL PEPTIDE FOR THE  
SEQUENCE FROM ompARBS = RIBOSOMAL  
BINDING SEQUENCEP<sub>R</sub> = "RIGHT" PROMOTOR FROM COLIPHAGE λcI857 THE GENE FOR A HEAT-SENSITIVE REPRES-  
SOR-PROTEIN FROM COLIPHAGE λ

## MULTIPLE CLONING SEQUENCE

NarI  
BglII  
EcoRI  
SacI  
KpnI  
XmaI  
BamHI  
XbaI  
SalI  
PstI  
SphIUNIQUE  
CLEAVING  
SITES

FIG. 1 PLASMA pHD 389. THE RIBOSOMAL BINDING-SEQUENCE (EMPHASIZED WITH A FULL LINE), THE SEQUENCE FOR SIGNAL PEPTIDE FROM ompA (FROM E.coli) (DOTTED LINE) AND RECOGNITION SEQUENCE FOR SEVERAL RESTRICTION ENZYMES ARE SHOWN.



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V V V V V V  
 GCATACAGATATGCAGATGCAATTAAGAAGGACAATGGAGAAATATACAGTAGACGTTGCA 420  
 AlaTyrArgTyrAlaAspAlaLeuLysLysAspAsnGlyGluTyrThrValAspValAla 140  
 V V V V V  
 GATAAAGGTTACTTTAAATATTAATTTGCTGGAAAAGAAAAAACACACAGAAACCA 480  
 AspLysGlyTyrThrLeuAsnIleLysPheAlaGlyLysGluLysThrProGluGluPro 160  
 V V V V V  
 AAAGAAGAAGTTACTATTAAGCAAACTTAATCTATGCAGATGGAAAAACACAAACAGCA 540  
 LysGluGluValThrIleLysAlaAsnLeuIleTyrAlaAspGlyLysThrGlnThrAla 180  
 V V V V V  
 GAATTCAAAGGAACATTTGAAGAAGCAACAGCAGCAAGCATAACAGATATGCTGACTTATTA 600  
 GluPheLysGlyThrPheGluGluAlaThrAlaGluAlaTyrArgTyrAlaAspLeuLeu 200  
 V V V V V  
 GCAAAGAAATGGTAAATATACAGTAGACGTTGCAGATAAAGGTTATACCTTTAAATATT 660  
 AlaLysGluAsnGlyLysTyrThrValaspValAlaAspLysGlyTyrThrLeuAsnIle 220  
 V V V V V  
 AAATTGCTGGA<sup>B4</sup>AAAGAAAAAACACACAGAAAGAACCAAAAGAAAGTACTATTAAAGCA 720  
 LysPheAlaGlyLysGluLysThrProGluGluProLysGluGluValThrIleLysAla 240  
 V V V V V  
 AACTTAATCTATGCAGATGGAAAAA<sup>B3</sup>CTCAAACAGCAGAGTTCAAAGGAACATTTGCAGAA 780  
 AsnLeuIleTyrAlaAspGlyLysThrGlnThrAlaGluPheLysGlyThrPheAlaGlu 260  
 (CONT.)

FIG. 2  
(CONT.)

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FIG. 2  
(CONT.)

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V V V V V V V  
 AAACCTGTTATTAATGGTAAACATTTGAAAGGCGGAAACAACACTAAAGCAGTAGACGCA 1200  
 LysLeuValIleAsnGlyLysThrLeuLysGlyGluThrThrThrLysAlaValAspAla 400

V V V V V V V  
 GAAACTGCAGAAAAAGCCCTTCAAAACAATACGCTAACGACAACGGTGTGATGGTGTGG 1260  
 GluThrAlaGluLysAlaPheLysGlnTyrAlaAsnAspAsnGlyValAspGlyValTrp 420

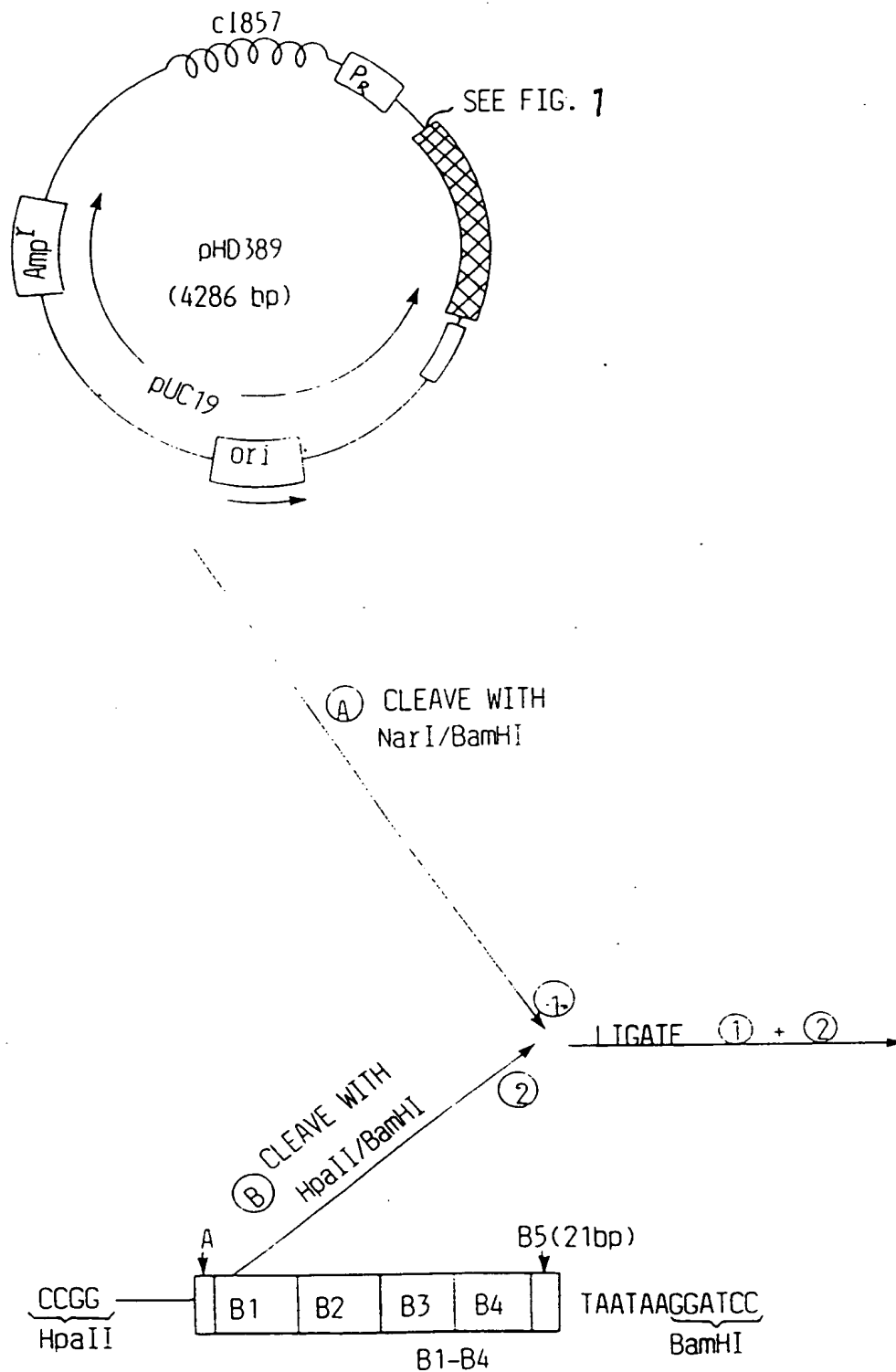
V V V V V  
 ACTTATGATGCGACTAAGACCTTTACGGTAACTGAAATGTAATAA 1308  
 ThrTyrAspAspAlaThrLysThrPheThrValThrGluMet - - 434

FIG. 2

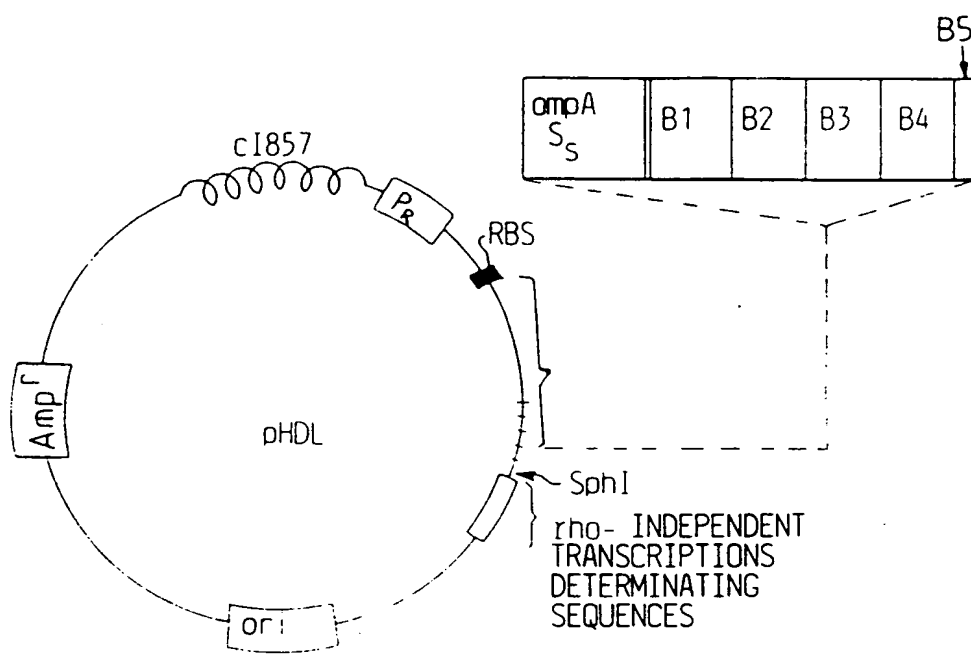


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FIG. 3 SCHEMATIC OVERALL VIEW OF THE PRODUCTION OF PROTEIN L



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TRANSFORM  
TO E.coli  
STRAIN LE392

FIG.3(2)

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FIG. 4

SCHEMATIC OVERALL VIEW OF PRODUCTION OF PROTEIN LG

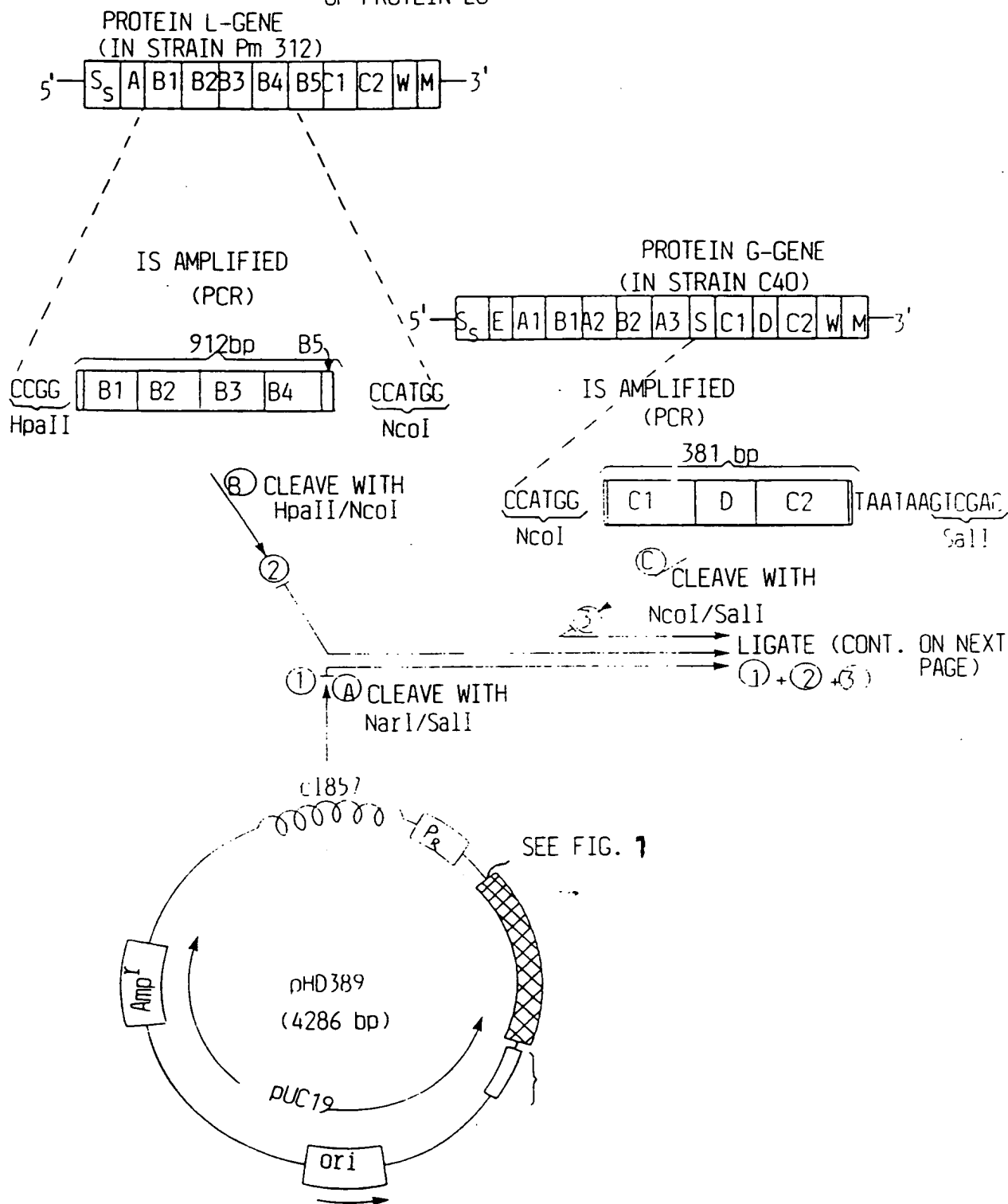
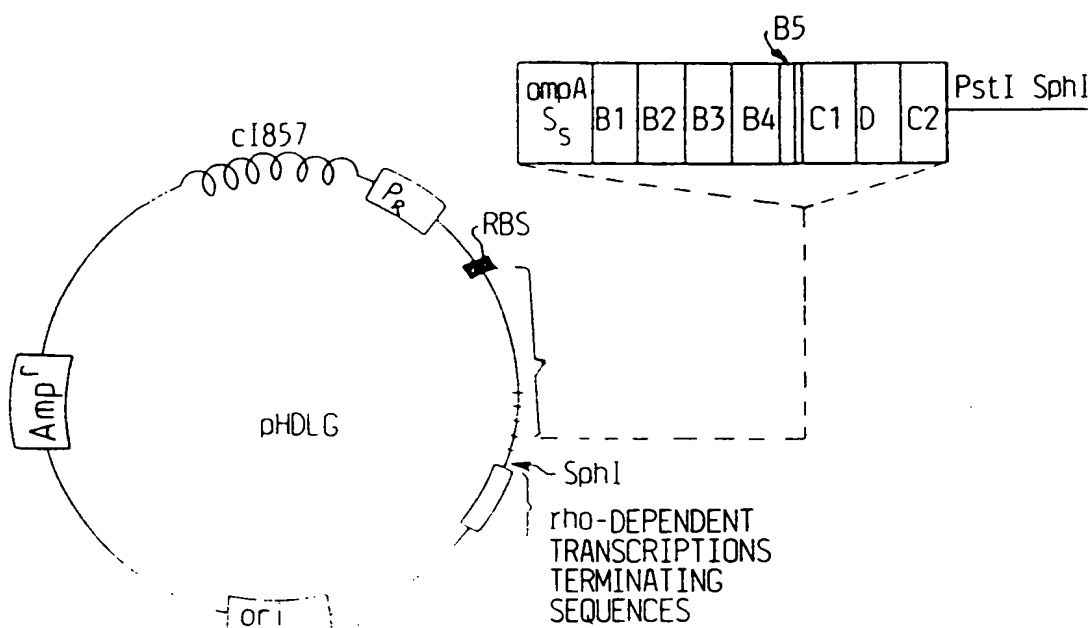


FIG.4(1)



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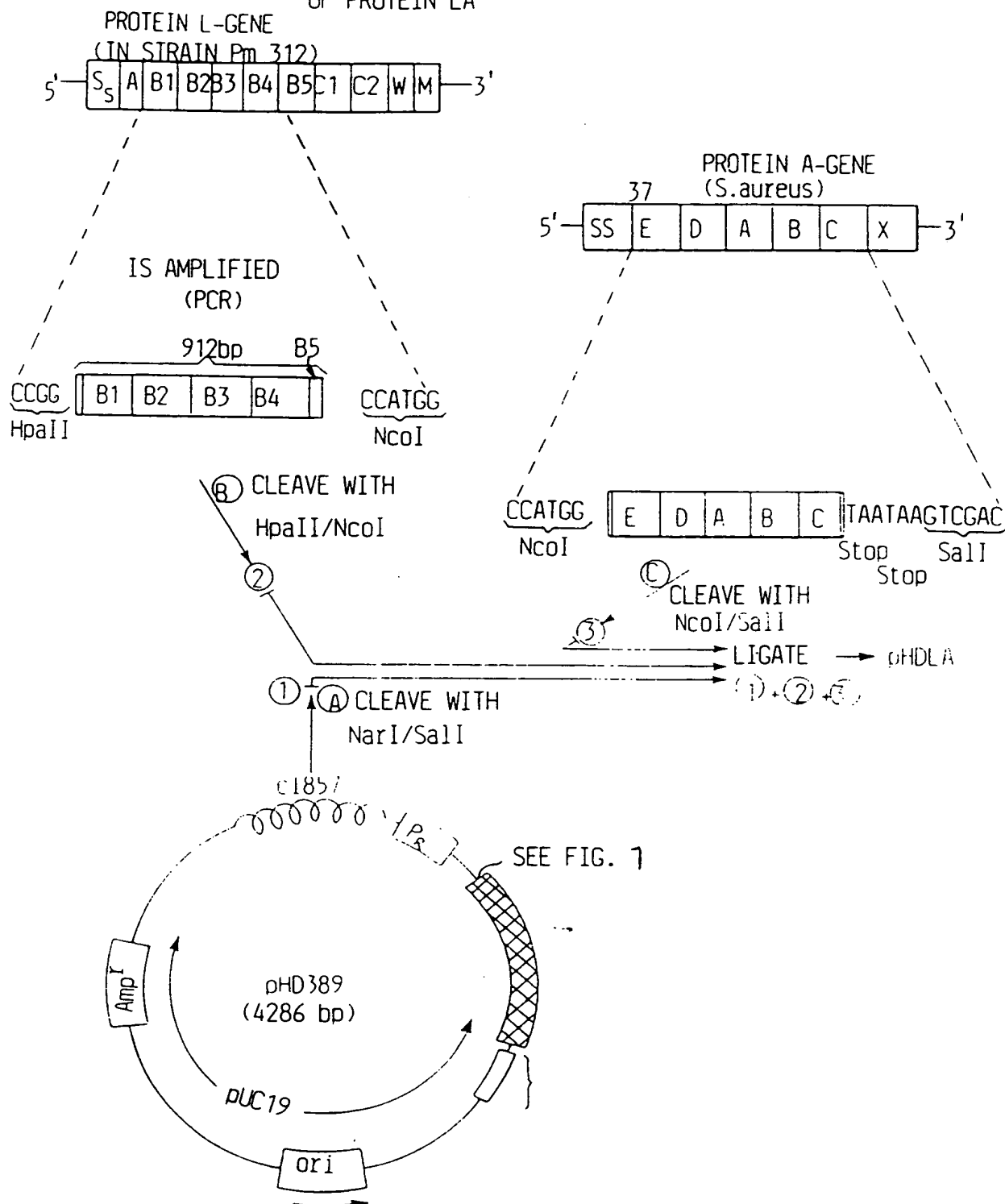


TRANSFORM  
TO *E. coli*  
STRAIN LE392

FIG.4(2)

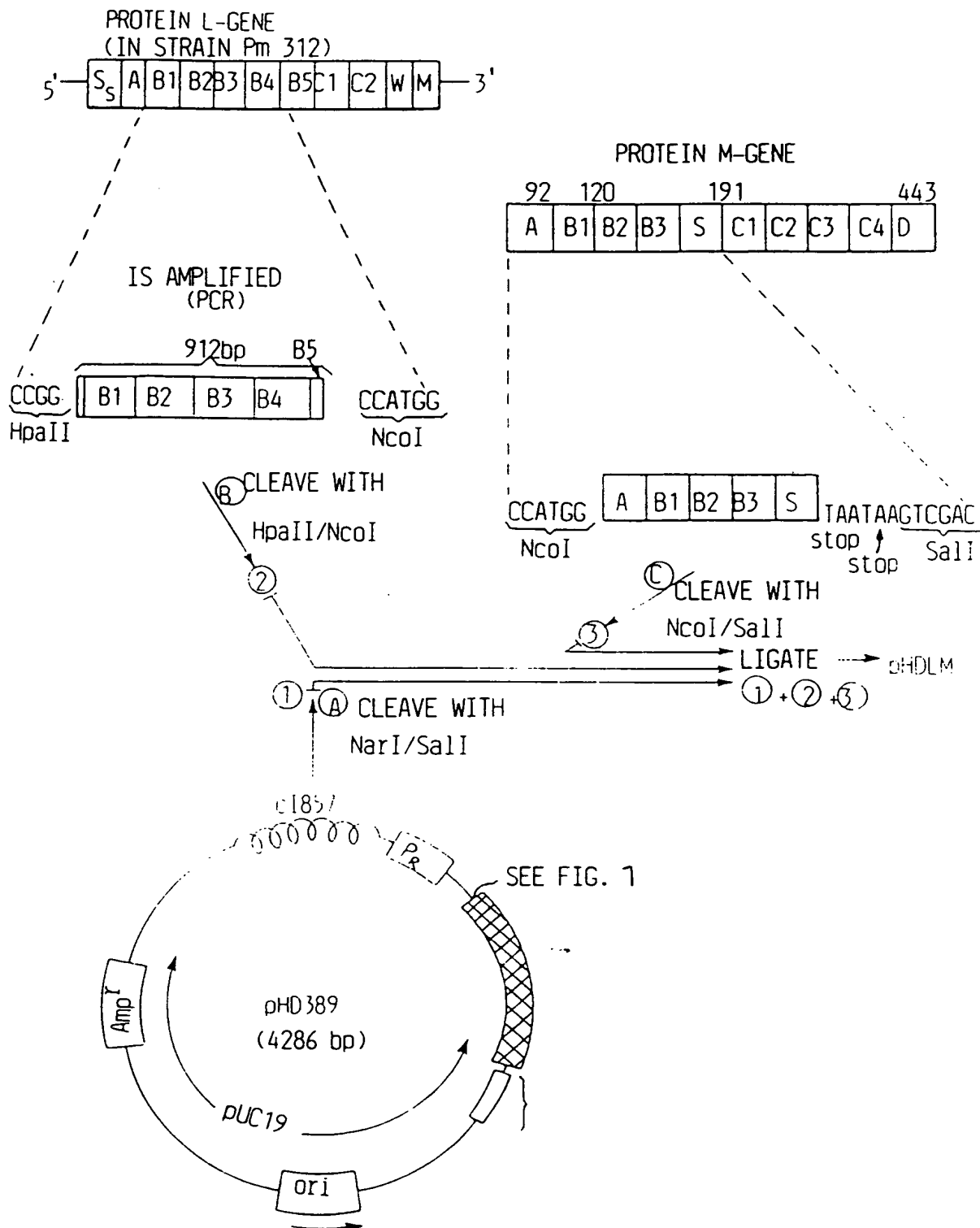
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FIG. 5a

SCHEMATIC OVERALL VIEW OF THE PRODUCTION  
OF PROTEIN LA

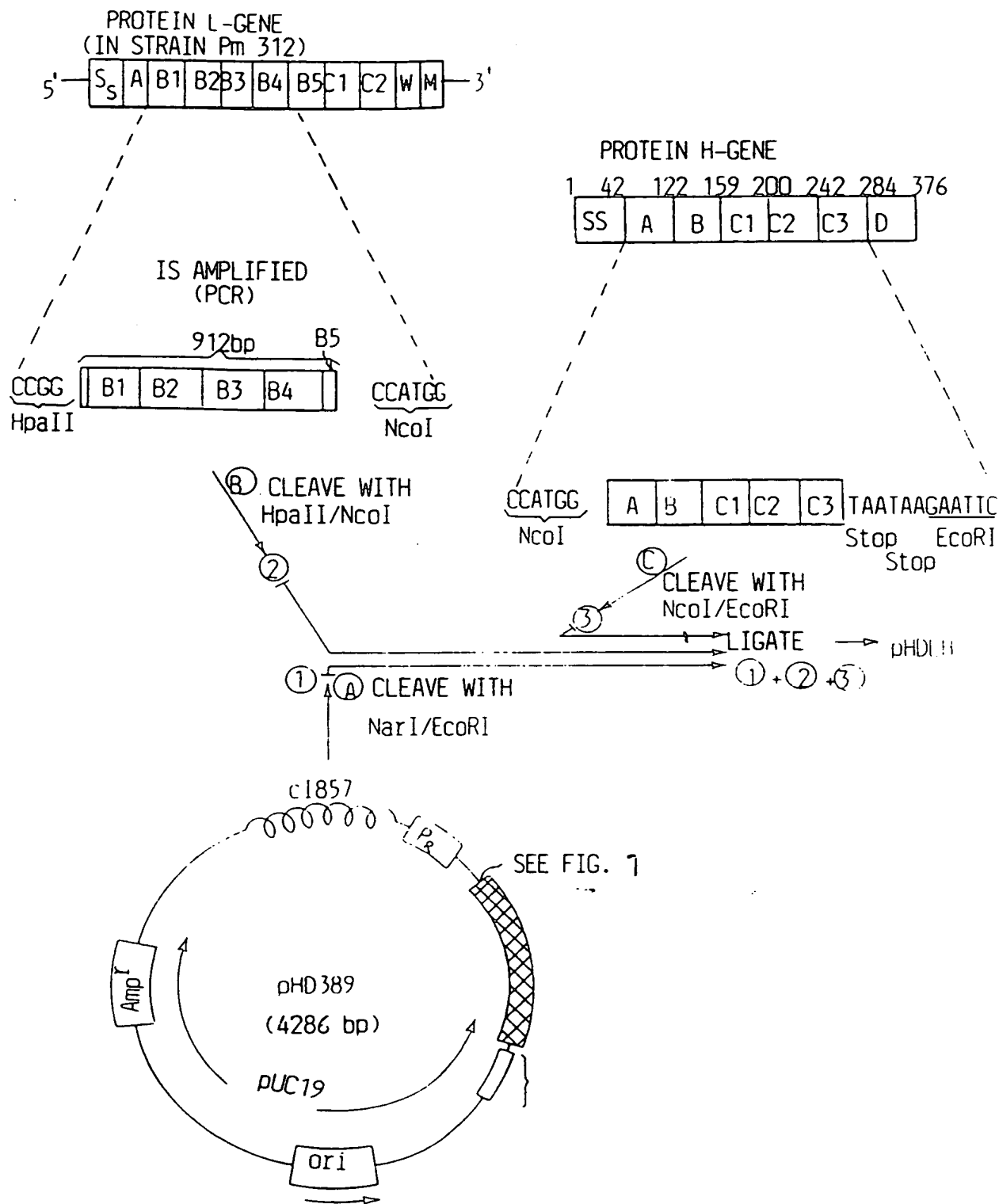
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FIG. 5b SCHEMATIC OVERALL VIEW OF THE PRODUCTION OF PROTEIN LM



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FIG. 5c SCHEMATIC OVERALL VIEW OF THE PRODUCTION OF PROTEIN LH



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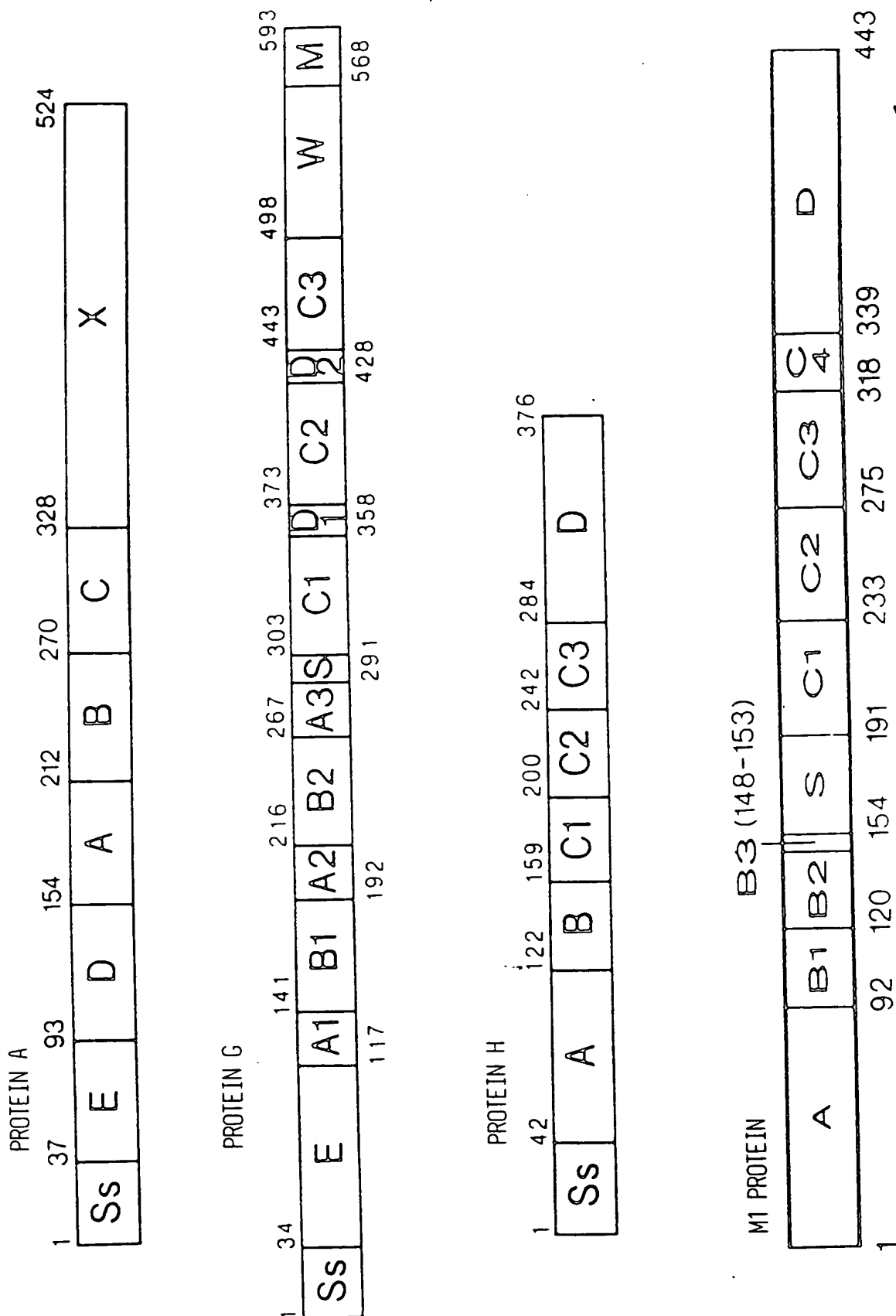


FIG.6

AACGGTGATGGTAATCCTAGGGAAGTTATAGAGATCTTGCAGCAACAAATCCCGCAATA  
 AsnGlyAspGlyAsnProArgGluValIleGluAspLeuAlaIleAsnAsnProAlaIle  
 60 20  
 CAAAATATACGTTTACGTCACGAAACACAGGACTTAAAGCGGAGATTAGAGAAATGCAATG  
 GlnAsnIleArgLeuArgHisGluAsnLysAspLeuLysAlaArgLeuGluAsnAlaMet  
 120 40  
 GAAGTTGCAGGAAGAGATTTTAAAGAGAGCTGAAGAACTTGAAAGCAAAACAAAGCCTTA  
 GluValAlaGlyArgAspPheLysArgAlaGluGluLeuGluLysAlaLysGlnAlaLeu  
 180 60  
 GAAGACCAGCGTAAGAGATTTAGAACTAAATTAAGAACTACACAAAGACTATGACTTA  
 GluAspGlnArgLysAspLeuGluThrLysLeuLysGluLeuGlnGlnAspTyrAspLeu  
 240 80  
 GCAAGGGAATCAACAAGTTGGGATAGACAAAGACTTGAAAGAGGTTAGAGAGAGAAAAG  
 AlaLysGluSerThrSerTrpAspArgGlnArgLeuGluLysGluLeuGluGluLysLys  
 300 100  
 GAAGCTCTTGAATTAGCGATAGACCAGGCAAGTCGGGACTACCATAGAGCTACCGCTTTA  
 GluAlaLeuGluLeuAlaIleAspGlnAlaSerArgAspTyrHisArgAlaThrAlaLeu  
 360 120  
 GAAAAAGAGTTAGAGAGAGAAAGAAAGCTCTTGAATTAGCGATAGACCAAGCGAGTCAG  
 GluLysGluLeuGluGluLysLysLysAlaLeuGluLeuAlaIleAspGlnAlaSerGln  
 420 140  
 GACTATAATAGAGCTAACGCTCTTAGAAAAAGAGTTAGAAACGATTACTAGAGAACAGAG  
 AspTyrAsnArgAlaAsnValLeuGluLysGluLeuGluThrIleThrArgGluGlnGlu  
 480 160  
 ATTAATCGTAATCTTTTAGGCAATGCAAACTTGAACTTGATCAACTTTCATCTGAAAAA  
 IleAsnArgAsnLeuLeuGluGlyAsnAlaLysLeuGluLeuAspGlnLeuSerSerGluLys  
 540 180

FIG. 7 (CONT.)

FIG. 7 (CONT.)

Amino acid sequence and nucleic acid sequence for protein M1, IgG-binding somewhere between amino acid 1-190.

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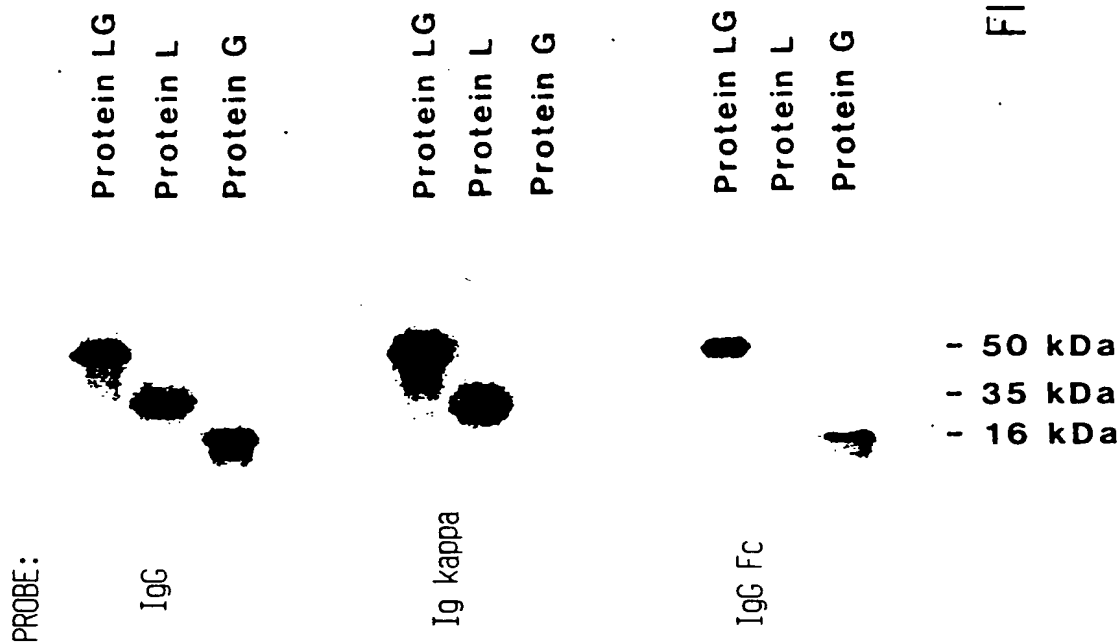
GAAAAGATTAGCAAACTTGACTGCTGAACCTTGATAAGGTTAAAGAGAGAAAACAAATC 840  
 GluLysAspLeuAlaAsnLeuThrAlaGluLeuAspLysValLysGluLysGlnIle 290  
 TCAGACGCAAGCCGTCACGGCTTCGCCGTGACTTGGACGCATCACGCTGAAGCTAAGAAA 900  
 SerAspAlaSerArgGlnArgLeuArgArgAspLeuAspAlaSerArgGluAlaLysLys 300  
 CAAGTTGAAAAGCTTTAGAAGAGCAACACAGCAAAATTAGCTGCTCTTGAAAAACTTAAC 960  
 GlnValGluLysAlaLeuGluGluAlaAsnSerLysLeuAlaAlaLeuGluLysLeuAsn 320  
 AAAGAGCTTGAAAGCAAGAAATTAAACAGAAAAGAAAAGCTGAACCTACAAGCAAAA 1020  
 LysGluLeuGluSerLysLysLeuThrGluLysGluLysAlaGluLeuGlnAlaLys 340  
 CTTGAAGCAGAAAGCAAAAGCACTCAAGAAACAATTAGCGAAACAAGCTGAAGAACTCGCA 1080  
 LeuGluAlaGluAlaLysAlaLeuLysGluGlnLeuAlaLysGlnAlaGluLeuAla 360  
 AAATAAGAGCTGGAAAAGCATCAGACTCACAACCCCTGATACAAACCAAGGAAACAAA 1140  
 LysLeuArgAlaGluLysAlaSerAspSerGlnThrProAspThrLysProGluAsnLys 380  
 GCTGTTCCAGGTAAAGGTCAAGCACCACAGCAGGTACAAACCTAACCAAAACAAGCA 1200  
 AlaValProGluLysGluGlnAlaProGlnAlaGluThrLysProAsnGlnAsnLysAla 400  
 CCAATGAAGGAACCTAAGAGACAGTTACCATCAACAGGTGAACAGCTAACCCATTCTTC 1260  
 ProMetLysGluThrLysArgGlnLeuProSerThrGluGluThrAlaAsnProPhe 420  
 ACAGCGGCACGCGTTACTGTTATGGCAACAGCTGGAGTAGCAGCAGTTGTAAACGCAAA 1320  
 ThrAlaAlaArgValThrValMetAlaThrAlaGluValAlaAlaValValLysArgLys 440

FIG. 7

GAAGAAAACCTAA 1329  
 GluGluAsn >>> 443



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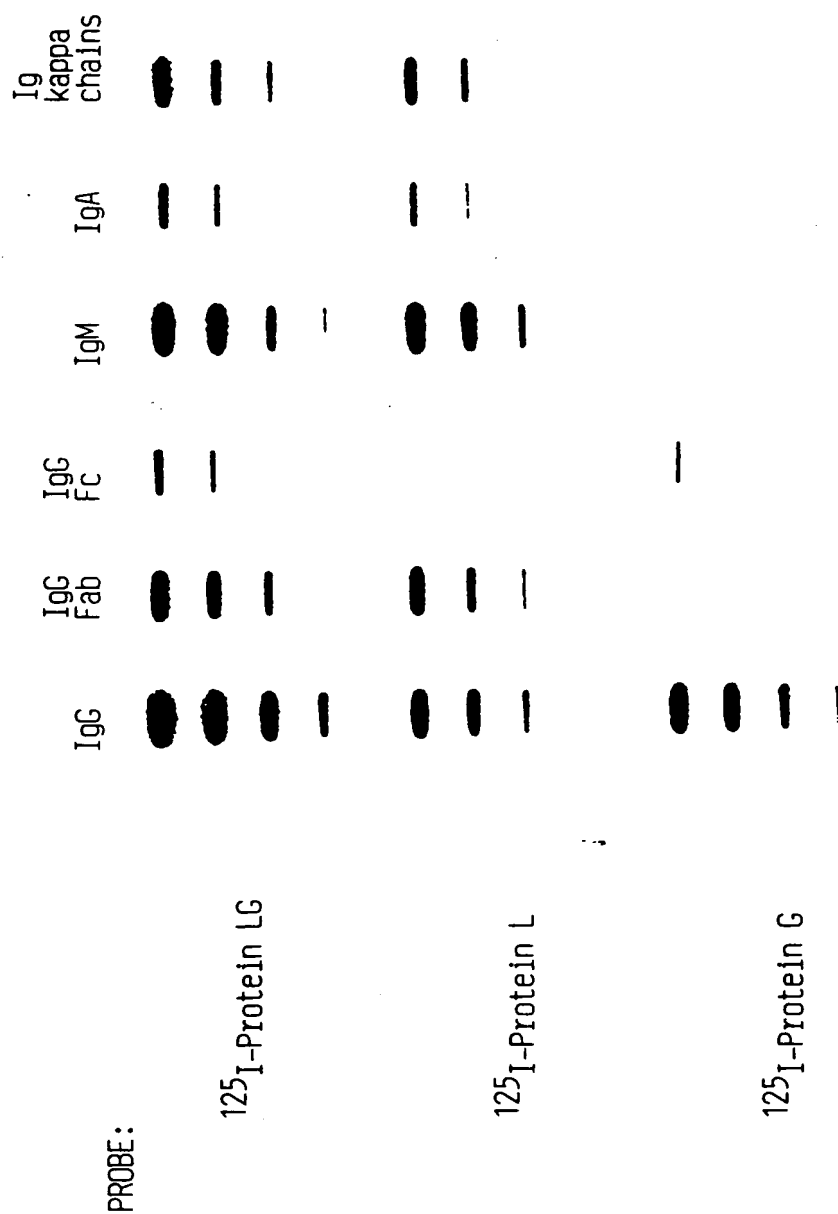


FIG. 9